What is claimed is:

1. A heteromeric variable region having higher antigen binding affinity than a donor heteromeric variable region, wherein said donor heteromeric variable region comprises three light chain donor CDRs and three heavy chain donor CDRs, and wherein said heteromeric variable region comprises:

a) a light chain altered variable region comprising;

i) four unvaried human germline light chain framework regions, wherein three of said four unvaried human germline light chain framework regions are from a human kappa light chain gene selected from the group consisting of: A11, A17, A18, A19, A20, A27, A30, L1, L11, L12, L2, L5, L6, L8, O12, O2, and O8; and

ii) three light chain altered variable region CDRs, wherein at least one of said three light chain altered variable region CDRs is a light chain donor CDR variant, and wherein said light chain donor CDR variant comprises a different amino acid at only one, two, three or four positions compared to one of said three light chain donor CDRs, and

b) a heavy chain altered variable region comprising;

i) four unvaried human germline heavy chain framework regions, wherein three of the four unvaried human germline heavy chain framework regions are from a human heavy chain gene selected from the group consisting of: VH2-5, VH2-26, VH2-70, VH3-20, VH3-72, VH1-46, VH3-9, VH3-66, VH3-74, VH4-31, VH1-18, VH1-69, VH3-7, VH3-11, VH3-15, VH3-21, VH3-23, VH3-30, VH3-48, VH4-39, VH4-59, and VH5-51; and

ii) three heavy chain altered variable region CDRs, wherein at least one of said three heavy chain altered variable region CDRs is a heavy chain donor CDR variant, and wherein said heavy chain donor CDR variant comprises a different amino acid at only one, two, three, or four positions compared to one of said three heavy chain donor CDRs.

2. The heteromeric variable region of Claim 1, wherein one of said three light chain altered variable region CDRs is identical to one of said three light chain donor CDRs.

3. The heteromeric variable region of Claim 1, wherein two of said three light chain altered variable region CDRs are each identical to one of said three light chain donor CDRs.

4. The heteromeric variable region of Claim 1, wherein one of said three heavy chain altered variable region CDRs is identical to one of said three heavy chain donor CDRs.

5. The heteromeric variable region of Claim 1, wherein two of said three heavy chain altered variable region CDRs are each identical to one of said three light chain donor CDRs.

6. The heteromeric variable region of Claim 1, wherein at least two of said three light chain altered variable region CDRs are light chain donor CDR variants.

7. The heteromeric variable region of Claim 1, wherein three of said three light chain altered variable region CDRs are light chain donor CDR variants.

8. The heteromeric variable region of Claim 1, wherein at least two of said three heavy chain altered variable region CDRs are heavy chain donor CDR variants.

9. The heteromeric variable region of Claim 1, wherein three of said three heavy chain altered variable region CDRs are heavy chain donor CDR variants.

10. The heteromeric variable region of Claim 1, wherein said donor heteromeric variable region is murine.

11. The heteromeric variable region of Claim 1, wherein said higher antigen binding affinity is at least 2-fold higher than the affinity of said donor heteromeric variable region.

12. The heteromeric variable region of Claim 1, wherein said higher antigen binding affinity is at least 3-fold higher than the affinity of said donor heteromeric variable region.

13. A method of expressing a heteromeric variable region having higher antigen binding affinity than a donor heteromeric variable region, wherein said donor heteromeric variable region comprises three light chain donor CDRs and three heavy chain donor CDRs, and wherein said method comprises;

a) providing;

i) a first oligonucleotide encoding an altered light chain variable region, wherein said altered light chain variable region comprises:

A) four unvaried human germline light chain framework regions, wherein three of said four unvaried human germline light chain framework regions are from a human kappa light chain gene selected from the group consisting of: A11, A17, A18, A19, A20, A27, A30, L1, L11, L12, L2, L5, L6, L8, O12, O2, and O8; and

B) three light chain altered variable region CDRs, wherein at least one of said three light chain altered variable region CDRs is a light chain donor CDR variant, and wherein said light chain donor CDR variant comprises a different amino acid at only one, two, three or four positions compared to one of said three light chain donor CDRs, and

ii) a second oligonucleotide encoding an altered heavy chain variable region, wherein said altered heavy chain variable region comprises;

A) four unvaried human germline heavy chain framework regions, wherein three of the four unvaried human germline heavy chain framework regions are from a human heavy chain gene selected from the group consisting of: VH2-5, VH2-26, VH2-70, VH3-20, VH3-72, VH1-46, VH3-9, VH3-66, VH3-74, VH4-31, VH1-18, VH1-69, VH3-7, VH3-11, VH3-15, VH3-21, VH3-23, VH3-30, VH3-48, VH4-39, VH4-59, and VH5-51; and

B) three heavy chain altered variable region CDRs, wherein at least one of said three heavy chain altered variable region CDRs is a heavy chain donor CDR variant, and wherein said heavy chain donor CDR variant comprises a different amino acid at only one, two, three, or four positions compared to one of said heavy chain donor CDRs, and

b) expressing said first and second oligonucleotides under conditions such that a heteromeric variable region binding fragment is generated that exhibits higher antigen binding affinity than said donor heteromeric variable region.

14. The method of Claim 13, wherein said expressing is coexpressing.

15. The method of Claim 13, wherein said higher antigen binding affinity is at least 2-fold higher than the affinity of said donor heteromeric variable region.

16. The method of Claim 13, wherein said higher antigen binding affinity is at least 3-fold higher than the affinity of said donor heteromeric variable region.

17. A method of expressing a heteromeric variable region having higher antigen binding affinity than a donor heteromeric variable region, wherein said donor heteromeric variable region comprises three light chain donor CDRs and three heavy chain donor CDRs, said method comprising;

a) providing;

i) first oligonucleotides encoding four unvaried human germline light chain framework regions, wherein three of said four unvaried human germline light chain framework regions are from a human kappa light chain gene selected from the group consisting of: A11, A17, A18, A19, A20, A27, A30, L1, L11, L12, L2, L5, L6, L8, O12, O2, and O8;

ii) a population of second oligonucleotides encoding:

A) first light chain CDRs, wherein said first light chain CDRs comprise donor CDR variants, wherein said donor CDR variants comprise a different amino acid at only one, two, three or four positions compared to one of said three light chain donor CDRs,

B) second light chain CDRs, wherein said second light chain CDRs encode each of said three light chain donor CDRs;

iii) third oligonucleotides encoding four unvaried human germline heavy chain framework regions, wherein three of the four unvaried human germline heavy chain framework regions are from a human heavy chain gene selected from the group consisting of: VH2-5, VH2-26, VH2-70, VH3-20, VH3-72, VH1-46, VH3-9, VH3-66, VH3-74, VH4-31, VH1-18, VH1-69, VH3-7, VH3-11, VH3-15, VH3-21, VH3-23, VH3-30, VH3-48, VH4-39, VH4-59, and VH5-51; and

iv) a population of fourth oligonucleotides encoding:

A) first heavy chain CDRs, wherein said first heavy chain CDRs comprise donor CDR variants, wherein said donor CDR variants comprise a different amino acid at only one, two, three or four positions compared to one of said three heavy chain donor CDRs, and

B) second heavy chain CDRs, wherein said second heavy chain CDRs encode each of said three heavy chain donor CDRs;

b) mixing said first oligonucleotides and said population of second oligoncucleotides such that a population of fifth oligonucleotides encoding light chain variable regions is generated, wherein at least one of said light chain variable regions encoded by said population of fifth oligonucleotides comprises i) an unvaried human germline light chain framework, and ii) at least one light chain donor CDR variant;

c) mixing said third oligonucleotides and said population of fourth oligonucleotides such that a population of sixth oligonucleotides encoding heavy chain variable regions is generated, wherein at least one of said heavy chain variable regions encoded by said population of sixth oligonucleotides comprises; i) an unvaried human germline heavy chain framework, and ii) at least one heavy chain donor CDR variant; and

d) expressing said fifth and sixth populations of oligonucleotides to produce combinations of heteromeric variable region binding fragments.

18. The method of Claim 17, further comprising step e) identifying at least one heteromeric variable region having higher antigen binding affinity than said donor heteromeric variable region.

19. The method of Claim 17, wherein said unvaried human germline light chain framework regions comprises FR1, FR2, FR3 and FR4 regions configured to hybridize to said light chain donor CDRs and said light chain donor CDR variants such that said population of fifth oligonucleotides encoding light chain variable regions is generated.

20. The method of Claim 17, wherein said unvaried human germline heavy chain framework regions comprises FR1, FR2, FR3 and FR4 regions configured to hybridize to said heavy chain donor CDRs and said heavy chain donor CDR variants such that said population of fifth oligonucleotides encoding heavy chain variable regions is generated.